



SEQUENCE LISTING

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Prayaga, Souminder K

(1) Novel Polypeptide Having Amino Acid Residues

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(163) 13

(170) PatentIn Ver. 3.1

(210) 1
(211) 633
(212) DNA
(213) Homo sapiens

(220)
(221) CDS
(222) (1)...(633)

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Phe Gly Val Val Val Gly Val Gly Ile Leu Ile Ile Ile Ile Ile Gly Ile

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Phe Gly Val Val Val Gly Val Gly Ile Leu Ile Ile Ile Ile Ile Gly Ile
4 8

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Leu Gly Ala Glu Val Gly Ser His Phe Leu Leu His His Ala Gly 111
112

Arg His His Leu Leu Gly His Arg Arg Ser Ala Ala His Arg Ser Ala
113 114

Asp Gly Gly His Gly Ala Ala His Leu Ala His Leu His Gly His His
115 116

Arg Arg Arg Glu Leu Tyr Tyr Arg Thr Gly His His Leu His His His
117 118

Pro Asp Gly Ser Val Glu Gly Thr Arg His Arg His Ser Leu His Gly
119 120

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser His Arg Gly
121 122

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly His Leu Tyr
123 124

Gly Ser Glu Lys Leu Thr Ser Glu Cys His Phe Arg His His Phe His
125 126

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn His Tyr Lys His Gly Asp
127 128

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Phe Arg
129 130

Asp Gly Ala Arg Ser Lys Arg His Glu Lys Phe Thr His Phe Leu His
131 132

Arg Pro Val Asp Pro Glu Arg Val Pro His Leu Tyr Lys Arg Leu Leu
133 134

Arg Tyr Thr
135

136
137
138

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<213> Artificial Sequence

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<213> Homo sapiens

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tctacctcgg gatgaatgag aagggggagc tgtatggatc agaaaacta acccaagggt 240
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ctt

414

Gly Leu Tyr Leu Gly Met Asn Glu Lys Tyr Glu Leu Tyr Gly Ser Thr
 114 115 116

Lys Leu Thr Val Ala Tyr Val Phe Asn Glu Ser Phe Val Glu Asn Lys
 117 118 119

Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Asn
 120 121 122

Asn Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Phe Asn Thr Gly Thr
 123 124 125

Asn Thr Lys Asn His Glu Lys Phe Thr His His Leu Leu Asn His Val
 126 127 128

Asp Phe Asp Lys Val Phe Glu Leu Tyr Lys Asp His Leu Ser Glu Ser
 129 130

<210> 10
 <211> 208
 <212> PRT
 <213> Mus sp.

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Val His Phe Gly Asn Val Phe Val Leu His Val Asp Ser His Val Lys
 11 12 13 14 15 16 17 18 19 20

Leu Asn Asp His Leu Gly His Ser Glu Asn Thr Gly Leu Thr Tyr
 21 22 23 24 25 26 27 28 29 30

Leu His Thr Asp Thr Ser His Leu Thr Ser Thr Ser Thr Ser Thr
 31 32 33 34 35 36 37 38 39 40

Glu Leu Tyr Tyr Asn Thr Gly His His Leu Glu His Thr Thr Asn Lys
 41 42 43 44 45 46 47 48 49 50

Leu Thr Val Gly Thr Asn Thr Asn His Leu Thr Thr Thr Thr Thr

Sly Lea Tyr Le Sly Met Ala Sly Lys Sly Val Lea Tyr Sly Met Ala
111 112 113

Lys Lea Thr Val Sly Tyr Val Sly Ala Sly Val Sly Val Sly Ala Tyr
114 115 116

Tyr Ala Thr Tyr Val Ser Ala Lea Tyr Lys His Val Asp Thr Sly Ala
117 118 119

Ala Tyr Tyr Val Ala Lea Ala Lys Asp Sly His Le Ala Ala Sly Thr
120 121 122

Ala Thr Lys Ala His Ala Lys Le Thr His Le Lea Le Ala Le Val
123 124 125

Asp His Asp Lys Val Le Ala Lea Tyr Lys Asp His Le Ser His Ala
126 127 128

+21 - 11
+211 - 2.5
+212 - FET
+213 - Rattus sp.

+400 - 11
Met Ala His Lea Sly His Val Sly Ser Tyr His Sly Val His Asp Ala
1 2 3 4 5 6 7 8 9 10

Val His His Sly Ala Val His Val Lea His Val Asp Ser His Val Lea
11 12 13 14 15 16 17 18 19 20

+1000 - 11
Met Ala His Lea Sly His Val Sly Ser Tyr His Sly Val His Asp Ala
1 2 3 4 5 6 7 8 9 10

+1000 - 11
Met Ala His Lea Sly His Val Sly Ser Tyr His Sly Val His Asp Ala
1 2 3 4 5 6 7 8 9 10

His Lea Tyr Tyr Ala Thr Sly His His Lea Ala His Ala Ala Tyr
1 2 3 4 5 6 7 8 9 10

Gly Leu Tyr Leu Gly Met Asn Lys Lys Gly Glu Lys Tyr Tyr Ser Glu
111 112 113

Lys Leu Thr Glu Glu Tyr Thr His Asn Lys Lys His Lys Lys Lys Lys
114 115 116 117 118 119 120 121 122 123 124 125 126 127 128

Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asn Thr Tyr Asn
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143

Arg Tyr Tyr Val Ala Leu Asn Lys Asn Lys Thr His Asn Lys Lys Lys
144 145 146 147 148 149 150 151 152 153 154 155 156 157 158

Arg Thr Lys Arg His Glu Lys His Thr His His Thr Lys Lys Val
159 160 161 162 163 164 165 166 167 168 169 170 171 172 173

Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asn His Lys Ser Glu Ser
174 175 176 177 178 179 180 181 182 183 184 185 186 187 188

<210> 12
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<212> PRT
<213> Xenopus sp.

<400> 12
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Leu Gly Glu Val Gly Ser His His Leu Leu His His Ala Lys Arg Ser
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His Leu Leu His Asn Asp His Thr Asn Lys Lys Lys Lys Lys Lys Lys
31 32 33 34 35 36 37 38 39 40 41 42 43 44 45

Asn Ala His Ser Asp Leu Ser His Leu His Lys Thr Thr Asn Asn Asn
46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

His Leu Lys Thr Asn His Lys Thr His Lys Lys Lys Lys Lys Lys Lys
61 62 63 64 65 66 67 68 69 70 71 72 73 74 75

